

# SEQUENCE LISTING

<110> Fraunhofer Gesellschaft zur Forderung der angewandten  
Forschung e.V.

<120> Immunokinases

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<141> 2005-01-13

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<151> 2004-01-16

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<151> 2004-07-29

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<170> PatentIn version 3.5

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open reading frame (ORF)

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gag gtg agc atc ctg cgg cag gtg ctg cac ccc aac atc atc acg ctg	336
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Gln Glu Ser Gly Thr Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met  
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Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp  
Page 8



50

55

60

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Pro Asn Thr Ala Tyr Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala  
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Asp Ser Phe Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
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Leu Leu Ile Tyr Gly Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg  
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Phe Ala Gly Ser Gly Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser  
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Val Gln Ala Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg  
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Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala  
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Ala Ala Leu Glu Ser Arg Met Val Gln Ala Ser Met Arg Ser Pro Asn  
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 Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser  
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 Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn  
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 Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn  
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 Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu  
 530 535 540  
 Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His  
 545 550 555 560  
 Pro Trp Ile Gly Ser Lys Leu Ala Glu His Glu Phe Arg Gly Gly Pro  
 565 570 575  
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His  
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 His His His His His  
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 <211> 3102  
 <212> DNA  
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1 5 10 15	
gcc cag ccg gcg atg gcc atg ggc cat cat cat cat cat cat cat cat	96
Ala Gln Pro Ala Met Ala Met Gly His His His His His His His His	
20 25 30	
cat cac agc agc ggc cat atc gac gac gac gac aag cat atg aag ctt	144
His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu	
35 40 45	
atg gcc cag ccg gcc atg gcc cag gtc aag ctg cag gag tca ggg act	192
Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr	
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gaa ctg gca aag cct ggg gcc gca gtg aag atg tcc tgc aag gct tct	240
Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser	
65 70 75 80	
ggc tac acc ttt act gac tac tgg atg cac tgg gtt aaa cag agg cct	288
Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro	
85 90 95	
gga cag ggt ctg gaa tgg att gga tac att aat cct aac act gct tat	336
Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr	
100 105 110	
act gac tac aat cag aaa ttc aag gac aag gcc aca ttg act gca gac	384
Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp	
115 120 125	
aaa tcc tcc agc aca gcc tac atg caa ctg cgc agc ctg acc tct gag	432
Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu	
130 135 140	
gat tct gca gtc tat tac tgt gca aaa aag aca act cag act acg tgg	480
Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp	
145 150 155 160	
ggg ttt cct ttt tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt	528
Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly	
165 170 175	
gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga tcg gac att	576
Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Gly Gly Gly Ser Asp Ile	
180 185 190	
gtg ctg acc cag tct cca aaa tcc atg gcc atg tca gtc gga gag agg	624

Val	Leu	Thr 195	Gln	Ser	Pro	Lys	Ser 200	Met	Ala	Met	Ser	Val 205	Gly	Glu	Arg	
gtc Val	acc Thr 210	ttg Leu	agc Ser	tgc Cys	aag Lys	gcc Ala 215	agt Ser	gag Glu	aat Asn	gtg Val	gat Asp 220	tct Ser	ttt Phe	gtt Val	tcc Ser	672
tgg Trp 225	tat Tyr	caa Gln	cag Gln	aaa Lys	cca Pro 230	ggc Gly	cag Gln	tct Ser	cct Pro	aaa Lys 235	ctg Leu	ctg Leu	ata Ile	tac Tyr	ggg Gly 240	720
gcc Ala	tcc Ser	aac Asn	cgg Arg	tac Tyr 245	act Thr	ggg Gly	gtc Val	ccc Pro	gat Asp 250	cgc Arg	ttc Phe	gca Ala	ggc Gly	agt Ser 255	gga Gly	768
tct Ser	gga Gly	aga Arg	gat Asp 260	ttc Phe	act Thr	ctg Leu	acc Thr	atc Ile 265	agc Ser	agt Ser	gtg Val	cag Gln	gct Ala 270	gaa Glu	gac Asp	816
ctt Leu	gca Ala	gat Asp 275	tat Tyr	cac His	tgt Cys	gga Gly	cag Gln 280	aat Asn	tac Tyr	agg Arg	tat Tyr	ccg Pro 285	ctc Leu	acg Thr	ttc Phe	864
ggc Gly	gct Ala 290	ggc Gly	acc Thr	aag Lys	ctg Leu	gaa Glu 295	atc Ile	aaa Lys	cgg Arg	gcg Ala	gcc Ala 300	gca Ala	gag Glu	ctc Leu	ggc Gly	912
gga Gly 305	ggt Gly	ggc Gly	tct Ser	atg Met	gca Ala 310	gac Asp	gaa Glu	gat Asp	ctc Leu	atc Ile 315	ttc Phe	cgc Arg	ctg Leu	gaa Glu	ggc Gly 320	960
gtt Val	gat Asp	ggc Gly	ggc Gly	cag Gln 325	tcc Ser	ccc Pro	cga Arg	gct Ala	ggc Gly 330	cat His	gat Asp	ggc Gly	gat Asp	tct Ser 335	gat Asp	1008
ggg Gly	gac Asp	agc Ser	gac Asp 340	gat Asp	gag Glu	gaa Glu	ggt Gly	tac Tyr 345	ttc Phe	atc Ile	tgc Cys	ccc Pro	atc Ile 350	acg Thr	gat Asp	1056
gac Asp	cca Pro	agc Ser 355	tcg Ser	aac Asn	cag Gln	aat Asn	gtc Val 360	aat Asn	tcc Ser	aag Lys	gtt Val	aat Asn 365	aag Lys	tac Tyr	tac Tyr	1104
agc Ser	aac Asn 370	cta Leu	aca Thr	aaa Lys	agt Ser	gag Glu 375	cgg Arg	tat Tyr	agc Ser	tcc Ser	agc Ser 380	ggg Gly	tcc Ser	ccg Pro	gca Ala	1152
aac Asn 385	tcc Ser	ttc Phe	cac His	ttc Phe	aag Lys 390	gaa Glu	gcc Ala	tgg Trp	aag Lys	cac His 395	gca Ala	atc Ile	cag Gln	aag Lys	gcc Ala 400	1200
aag Lys	cac His	atg Met	ccc Pro	gac Asp 405	ccc Pro	tgg Trp	gct Ala	gag Glu	ttc Phe 410	cac His	ctg Leu	gaa Glu	gat Asp	att Ile 415	gcc Ala	1248
acc Thr	gaa Glu	cgt Arg	gct Ala 420	act Thr	cga Arg	cac His	agg Arg	tac Tyr 425	aac Asn	gcc Ala	gtc Val	acc Thr	ggg Gly 430	gaa Glu	tgg Trp	1296
ctg Leu	gat Asp	gat Asp 435	gaa Glu	gtt Val	ctg Leu	atc Ile	aag Lys 440	atg Met	gca Ala	tct Ser	cag Gln	ccc Pro 445	ttc Phe	ggc Gly	cga Arg	1344
gga Gly	gca Ala 450	atg Met	agg Arg	gag Glu	tgc Cys	ttc Phe 455	cgg Arg	acg Thr	aag Lys	aag Lys	ctc Leu 460	tcc Ser	aac Asn	ttc Phe	ttg Leu	1392
cat His	gcc Ala	cag Gln	cag Gln	tgg Trp	aag Lys	ggc Gly	gcc Ala	tcc Ser	aac Asn	tac Tyr	gtg Val	gcg Ala	aag Lys	cgc Arg	tac Tyr	1440

465	470										475					480					
atc Ile	gag Glu	ccc Pro	gta Val	gac Asp 485	cgg Arg	gat Asp	gtg Val	tac Tyr	ttt Phe 490	gag Glu	gac Asp	gtg Val	cgt Arg	cta Leu 495	cag Gln	1488					
atg Met	gag Glu	gcc Ala	aag Lys 500	ctc Leu	tgg Trp	ggg Gly	gag Glu	gag Glu 505	tat Tyr	aat Asn	cgg Arg	cac His	aag Lys 510	ccc Pro	ccc Pro	1536					
aag Lys	cag Gln	gtg Val 515	gac Asp	atc Ile	atg Met	cag Gln	atg Met 520	tgc Cys	atc Ile	atc Ile	gag Glu	ctg Leu 525	aag Lys	gac Asp	aga Arg	1584					
ccg Pro	ggc Gly 530	aag Lys	ccc Pro	ctc Leu	ttc Phe	cac His 535	ctg Leu	gag Glu	cac His	tac Tyr	atc Ile 540	gag Glu	ggc Gly	aag Lys	tac Tyr	1632					
atc Ile 545	aag Lys	tac Tyr	aac Asn	tcc Ser	aac Asn 550	tct Ser	ggc Gly	ttt Phe	gtc Val	cgc Arg 555	gat Asp	gac Asp	aac Asn	atc Ile	cgc Arg 560	1680					
ctg Leu	acg Thr	ccg Pro	cag Gln	gcc Ala 565	ttc Phe	agc Ser	cac His	ttc Phe	act Thr 570	ttt Phe	gag Glu	cgt Arg	tcc Ser	ggc Gly 575	cat His	1728					
cag Gln	ctg Leu	ata Ile	gtg Val 580	gtg Val	gac Asp	atc Ile	cag Gln	gga Gly 585	gtt Val	ggg Gly	gat Asp	ctc Leu	tac Tyr 590	act Thr	gac Asp	1776					
cca Pro	cag Gln	atc Ile 595	cac His	acg Thr	gag Glu	acg Thr	ggc Gly 600	act Thr	gac Asp	ttt Phe	gga Gly	gac Asp 605	ggc Gly	aac Asn	cta Leu	1824					
ggt Gly	gtc Val 610	cgc Arg	ggg Gly	atg Met	gcg Ala	ctc Leu 615	ttc Phe	ttc Phe	tac Tyr	tct Ser	cat His 620	gcc Ala	tgc Cys	aac Asn	cgg Arg	1872					
att Ile 625	tgc Cys	gag Glu	agc Ser	atg Met	ggc Gly 630	ctt Leu	gct Ala	ccc Pro	ttt Phe	gac Asp 635	ctc Leu	tcg Ser	ccc Pro	cgg Arg	gag Glu 640	1920					
agg Arg	gat Asp	gca Ala	gtg Val	aat Asn 645	cag Gln	aac Asn	acc Thr	aag Lys	ctg Leu 650	ctg Leu	caa Gln	tca Ser	gcc Ala	aag Lys 655	acc Thr	1968					
atc Ile	ttg Leu	aga Arg	gga Gly 660	aca Thr	gag Glu	gaa Glu	aaa Lys	tgt Cys 665	ggg Gly	agc Ser	ccc Pro	cga Arg	gta Val 670	agg Arg	acc Thr	2016					
ctc Leu	tct Ser	ggg Gly 675	agc Ser	cgg Arg	cca Pro	ccc Pro	ctg Leu 680	ctc Leu	cgt Arg	ccc Pro	ctt Leu	tca Ser 685	gag Glu	aac Asn	tct Ser	2064					
gga Gly 690	gac Asp	gag Glu	aac Asn	atg Met	agc Ser	gac Asp 695	gtg Val	acc Thr	ttc Phe	gac Asp	tct Ser 700	ctc Leu	cct Pro	tct Ser	tcc Ser	2112					
cca Pro 705	tct Ser	tcg Ser	gcc Ala	aca Thr	cca Pro 710	cac His	agc Ser	cag Gln	aag Lys	cta Leu 715	gac Asp	cac His	ctc Leu	cat His	tgg Trp 720	2160					
cca Pro	gtc Val	ttc Phe	agt Ser	gac Asp 725	ctc Leu	gat Asp	aac Asn	atg Met	gca Ala 730	tcc Ser	aga Arg	gac Asp	cat His	gat Asp 735	cat His	2208					
cta Leu	gac Asp	aac Asn	cac His 740	cgg Arg	gag Glu	tct Ser	gag Glu	aat Asn 745	agt Ser	ggg Gly	gac Asp	agc Ser	gga Gly 750	tac Tyr	ccc Pro	2256					

agt gag aag cgg ggt gag ctg gat gac cct gag ccc cga gaa cat ggc Ser Glu Lys Arg Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly 755 760 765	2304
cac tca tac agt aat cgg aag tac gag tct gac gaa gac agc ctg ggc His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly 770 775 780	2352
agc tct gga cgg gta tgt gta gag aag tgg aat ctc ctc aac tcc tcc Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser 785 790 800	2400
cgc ctc cac ctg ccg agg gct tcg gcc gtg gcc ctg gaa gtg caa agg Arg Leu His Leu Pro 805 Arg Ala Ser Ala Val 810 Ala Leu Glu Val 815 Gln Arg	2448
ctt aat gct ctg gac ctc gaa aag aaa atc ggg aag tcc att ttg ggg Leu Asn Ala Leu 820 Asp Leu Glu Lys Lys 825 Ile Gly Lys Ser 830 Ile Leu Gly	2496
aag gtc cat ctg gcc atg gtg cgc tac cac gag ggt ggg cgc ttc tgc Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys 835 840 845	2544
gag aag ggc gag gag tgg gac cag gag tcg gct gtc ttc cac ctg gag Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu 850 855 860	2592
cac gca gcc aac ctg ggc gag ctg gag gcc atc gtg ggc ctg gga ctc His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu 865 870 875 880	2640
atg tac tcg cag ttg cct cat cac atc cta gcc gat gtc tct ctg aag Met Tyr Ser Gln Leu 885 Pro His His Ile Leu Ala Asp Val Ser Leu Lys 890 895	2688
gag aca gaa gag aac aaa acc aaa gga ttt gat tac tta cta aag gcc Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala 900 905 910	2736
gct gaa gct ggc gac agg cag tcc atg atc cta gtg gcg cga gct ttt Ala Glu Ala 915 Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe 920 925	2784
gac tct ggc cag aac ctc agc ccg gac agg tgc caa gac tgg cta gag Asp Ser 930 Gly Gln Asn Leu Ser 935 Pro Asp Arg Cys Gln 940 Asp Trp Leu Glu	2832
gcc ctg cac tgg tac aac act gcc ctg gag atg acg gac tgt gat gag Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu 945 950 955 960	2880
ggc ggt gag tac gac gga atg cag gac gag ccc cgg tac atg atg ctg Gly Gly Glu Tyr Asp 965 Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu 970 975	2928
gcc agg gag gcc gag atg ctg ttc aca gga ggc tac ggg ctg gag aag Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys 980 985 990	2976
gac ccg cag aga tca ggg gac ttg tat acc cag gca gca gag gca gcg Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala 995 1000 1005	3024
atg gaa gcc atg aag ggc cga ctg gcc aac cag tac tac caa aag Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys 1010 1015 1020	3069

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3102

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 <211> 1033  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Construct

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Ala Gln Pro Ala Met Ala Met Gly His His His His His His His His  
 20 25 30

His His Ser Ser Gly His Ile Asp Asp Asp Asp Lys His Met Lys Leu  
 35 40 45

Met Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Glu Ser Gly Thr  
 50 55 60

Glu Leu Ala Lys Pro Gly Ala Ala Val Lys Met Ser Cys Lys Ala Ser  
 65 70 75 80

Gly Tyr Thr Phe Thr Asp Tyr Trp Met His Trp Val Lys Gln Arg Pro  
 85 90 95

Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Asn Thr Ala Tyr  
 100 105 110

Thr Asp Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp  
 115 120 125

Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu  
 130 135 140

Asp Ser Ala Val Tyr Tyr Cys Ala Lys Lys Thr Thr Gln Thr Thr Trp  
 145 150 155 160

Gly Phe Pro Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly  
 165 170 175

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile  
 180 185 190

Val Leu Thr Gln Ser Pro Lys Ser Met Ala Met Ser Val Gly Glu Arg  
 195 200 205

Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Asp Ser Phe Val Ser  
 210 215 220

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Gly  
 225 230 235 240  
 Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Ala Gly Ser Gly  
 245 250 255  
 Ser Gly Arg Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp  
 260 265 270  
 Leu Ala Asp Tyr His Cys Gly Gln Asn Tyr Arg Tyr Pro Leu Thr Phe  
 275 280 285  
 Gly Ala Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu Leu Gly  
 290 295 300  
 Gly Gly Gly Ser Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly  
 305 310 315 320  
 Val Asp Gly Gly Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp  
 325 330 335  
 Gly Asp Ser Asp Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp  
 340 345 350  
 Asp Pro Ser Ser Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr  
 355 360 365  
 Ser Asn Leu Thr Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala  
 370 375 380  
 Asn Ser Phe His Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala  
 385 390 395 400  
 Lys His Met Pro Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala  
 405 410 415  
 Thr Glu Arg Ala Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp  
 420 425 430  
 Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg  
 435 440 445  
 Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu  
 450 455 460  
 His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr  
 465 470 475 480  
 Ile Glu Pro Val Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln  
 485 490 495



Met Glu Ala Lys<sub>500</sub> Leu Trp Gly Glu Glu<sub>505</sub> Tyr Asn Arg His Lys<sub>510</sub> Pro Pro  
 Lys Gln Val<sub>515</sub> Asp Ile Met Gln Met<sub>520</sub> Cys Ile Ile Glu Leu<sub>525</sub> Lys Asp Arg  
 Pro Gly<sub>530</sub> Lys Pro Leu Phe His<sub>535</sub> Leu Glu His Tyr Ile<sub>540</sub> Glu Gly Lys Tyr  
 Ile<sub>545</sub> Lys Tyr Asn Ser Asn<sub>550</sub> Ser Gly Phe Val Arg<sub>555</sub> Asp Asp Asn Ile Arg<sub>560</sub>  
 Leu Thr Pro Gln Ala<sub>565</sub> Phe Ser His Phe Thr<sub>570</sub> Phe Glu Arg Ser Gly<sub>575</sub> His  
 Gln Leu Ile Val<sub>580</sub> Val Asp Ile Gln Gly<sub>585</sub> Val Gly Asp Leu Tyr<sub>590</sub> Thr Asp  
 Pro Gln Ile<sub>595</sub> His Thr Glu Thr Gly<sub>600</sub> Thr Asp Phe Gly Asp<sub>605</sub> Gly Asn Leu  
 Gly Val<sub>610</sub> Arg Gly Met Ala Leu<sub>615</sub> Phe Phe Tyr Ser His<sub>620</sub> Ala Cys Asn Arg  
 Ile<sub>625</sub> Cys Glu Ser Met Gly<sub>630</sub> Leu Ala Pro Phe Asp<sub>635</sub> Leu Ser Pro Arg Glu<sub>640</sub>  
 Arg Asp Ala Val<sub>645</sub> Asn Gln Asn Thr Lys Leu<sub>650</sub> Leu Gln Ser Ala Lys<sub>655</sub> Thr  
 Ile Leu Arg Gly<sub>660</sub> Thr Glu Glu Lys Cys<sub>665</sub> Gly Ser Pro Arg Val<sub>670</sub> Arg Thr  
 Leu Ser Gly<sub>675</sub> Ser Arg Pro Pro Leu<sub>680</sub> Leu Arg Pro Leu Ser<sub>685</sub> Glu Asn Ser  
 Gly Asp<sub>690</sub> Glu Asn Met Ser Asp<sub>695</sub> Val Thr Phe Asp Ser<sub>700</sub> Leu Pro Ser Ser  
 Pro Ser Ser Ala Thr Pro<sub>710</sub> His Ser Gln Lys Leu<sub>715</sub> Asp His Leu His Trp<sub>720</sub>  
 Pro Val Phe Ser Asp<sub>725</sub> Leu Asp Asn Met Ala<sub>730</sub> Ser Arg Asp His Asp<sub>735</sub> His  
 Leu Asp Asn His<sub>740</sub> Arg Glu Ser Glu Asn<sub>745</sub> Ser Gly Asp Ser Gly<sub>750</sub> Tyr Pro  
 Ser Glu Lys<sub>755</sub> Arg Gly Glu Leu Asp<sub>760</sub> Asp Pro Glu Pro Arg<sub>765</sub> Glu His Gly

His Ser Tyr Ser Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly  
 770 775 780  
 Ser Ser Gly Arg Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser  
 785 790 795 800  
 Arg Leu His Leu Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg  
 805 810 815  
 Leu Asn Ala Leu Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly  
 820 825 830  
 Lys Val His Leu Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys  
 835 840 845  
 Glu Lys Gly Glu Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu  
 850 855 860  
 His Ala Ala Asn Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu  
 865 870 875 880  
 Met Tyr Ser Gln Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys  
 885 890 895  
 Glu Thr Glu Glu Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala  
 900 905 910  
 Ala Glu Ala Gly Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe  
 915 920 925  
 Asp Ser Gly Gln Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu  
 930 935 940  
 Ala Leu His Trp Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu  
 945 950 955 960  
 Gly Gly Glu Tyr Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu  
 965 970 975  
 Ala Arg Glu Ala Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys  
 980 985 990  
 Asp Pro Gln Arg Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala  
 995 1000 1005  
 Met Glu Ala Met Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys  
 1010 1015 1020  
 Ala Glu Glu Ala Trp Ala Gln Met Glu Glu  
 1025 1030

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<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic linker

<400> 7

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
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<210> 8  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> c-Myc epitope

<400> 8

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
1 5 10

<210> 9  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> motif in domain IX of kinases

<220>  
<221> Variant  
<222> (2)..(2)  
<223> Xaa is any amino acid

<220>  
<221> Variant  
<222> (4)..(5)  
<223> Xaa is any amino acid

<400> 9

Asp Xaa Trp Xaa Xaa Gly  
1 5